AMENDMENTS TO THE CLAIMS

In the Claims:

Please amend claim 56, add new claims 74-81, and cancel claims 1-55 and 57-73, as shown in the following listing of claims, which will replace all prior versions and listings of claims in the application. Claims 2, 4-6, 8, 14, and 20-25 were previously withdrawn. Please cancel claims 1-55 and 57-73 without prejudice to their pursuit in an appropriate continuation or divisional application. Claims 56 and 74-81 are presently in the application with claim 74 being the independent claim.

Listing of claims:

1. – 55. (canceled)

56 (currently amended). The ~~process according to claim 44~~method of claim 79, wherein the pre-sequence is enzymatically cleaved from the formed peptide.

57. – 73. (canceled)

74 (new). A method of using a selected pre-sequence to produce a peptide of interest with the following structure:

$$X\text{-}AA_1\text{-}AA_2\text{.....}AA_n\text{-}Y,$$

wherein,

(1) AA is an L or D amino acid residue,

(2) X is hydrogen or an amino protective group,

(3) Y is OH or NH_2, and

(4) n is an integer greater than about 2 and less than about 60;

and further wherein the method comprises the following steps:

a. selecting a pre-sequence comprising from about 3 to about 9 amino acid residues having side chain functionalities which are protected during the synthesis, wherein the amino acid residues are independently selected from the group consisting of: L-amino acids having a propensity factor $P_\alpha > 0.57$ and a propensity factor $P_\beta \leq 1.10$, and the corresponding D-amino acids,

b. coupling the pre-sequence to a support as follows:

i. coupling an N-α-protected C-terminal amino acid selected from step (a), to the support and subsequently removing the N-α-protecting group;

ii. coupling one or more amino acids selected from step (a) to the C-terminal amino acid from step b(i), wherein each coupling is performed in stepwise fashion and under conditions in which each amino acid is protected and subsequently de-protected, to form the pre-sequence;

iii. coupling one or more amino acids to the N-terminus of the pre-sequence to form the peptide of interest, wherein each coupling is performed in stepwise fashion and under conditions in which each of the amino acids of the peptide is coupled and subsequently N-α-de-protected; wherein the pre-sequence reduces or eliminates propensity of the peptide of interest to adopt a β-sheet structure during the coupling; and

c. cleaving at least the peptide of interest from the support to make the peptide.

75 (new). The method of claim 74, wherein AA further comprises a side-chain protecting group.

76 (new). The method of claim 74, wherein the pre-sequence comprises amino acid residues that lack propensity to adopt the β-sheet structure.

77 (new). The method of claim 74, wherein the method further comprises removing the N-α-protective group from the peptide of interest before step (c).

78 (new). The method of claim 74, wherein at step (c) the peptide of interest further comprises the pre-sequence.

79 (new). The method of claim 78, wherein the method further comprises cleaving the pre-sequence from the peptide.

80 (new). The method of claim 74, wherein the method further comprises at least one of the following steps: inserting a first linker between peptide of interest and the pre-sequence, and inserting a second linker between the pre-sequence and the support.

81 (new). The method of claim 80, wherein step (c) further comprises cleaving the first linker, the second linker or both the first and second linkers to produce the peptide of interest.